

SCORE Search Results Details for Application 08900220 and Search Result us-08-900-220c-17.rai.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 08900220 and Search Result us-08-900-220c-17.rai.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2006, 11:40:16 ; Search time 50 Seconds
(without alignments)
693.243 Million cell updates/sec

Title: US-08-900-220C-17
Perfect score: 2088
Sequence: 1 MALLTNLLPLCCLALLALPA.....PTGMHWYSRLLYRLABELLG 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2088	100.0	396	2	US-09-325-256-24	Sequence 24, Appl
2	2088	100.0	396	2	US-09-704-917-17	Sequence 17, Appl
3	2088	100.0	396	2	US-09-151-999-17	Sequence 17, Appl
4	2088	100.0	396	2	US-09-569-386-17	Sequence 17, Appl
5	2088	100.0	396	2	US-08-905-572A-17	Sequence 17, Appl
6	2088	100.0	396	2	US-09-724-964B-17	Sequence 17, Appl
7	2083	99.8	396	3	US-09-063-778-3	Sequence 3, Appli
8	2008	96.2	396	1	US-08-176-427B-4	Sequence 4, Appli
9	2008	96.2	396	1	US-08-356-060A-9	Sequence 9, Appli
10	2008	96.2	396	2	US-08-460-900C-9	Sequence 9, Appli

11	2008	96.2	396	2	US-08-674-509B-9	Sequence 9, Appli
12	2008	96.2	396	2	US-08-954-698-9	Sequence 9, Appli
13	2008	96.2	396	2	US-09-293-505-13	Sequence 13, Appli
14	2008	96.2	396	2	US-08-957-874-9	Sequence 9, Appli
15	2008	96.2	396	2	US-09-325-256-18	Sequence 18, Appli
16	2008	96.2	396	2	US-09-639-695-9	Sequence 9, Appli
17	2008	96.2	396	2	US-09-448-188-9	Sequence 9, Appli
18	2008	96.2	396	2	US-08-954-128-9	Sequence 9, Appli
19	2008	96.2	396	2	US-09-704-917-11	Sequence 11, Appli
20	2008	96.2	396	2	US-08-954-740-9	Sequence 9, Appli
21	2008	96.2	396	2	US-09-151-999-11	Sequence 11, Appli
22	2008	96.2	396	2	US-09-736-476-9	Sequence 9, Appli
23	2008	96.2	396	2	US-09-060-939A-13	Sequence 13, Appli
24	2008	96.2	396	2	US-09-021-660A-35	Sequence 35, Appli
25	2008	96.2	396	2	US-09-418-221-11	Sequence 11, Appli
26	2008	96.2	396	2	US-09-569-386-11	Sequence 11, Appli
27	2008	96.2	396	2	US-08-905-572A-11	Sequence 11, Appli
28	2008	96.2	396	2	US-09-733-634-22	Sequence 22, Appli
29	2008	96.2	396	2	US-09-724-964B-11	Sequence 11, Appli
30	1974	94.5	374	3	US-09-063-778-2	Sequence 2, Appli
31	1217	58.3	437	1	US-08-176-427B-8	Sequence 8, Appli
32	1217	58.3	437	1	US-08-356-060A-11	Sequence 11, Appli
33	1217	58.3	437	2	US-08-460-900C-11	Sequence 11, Appli
34	1217	58.3	437	2	US-08-674-509B-11	Sequence 11, Appli
35	1217	58.3	437	2	US-08-954-698-11	Sequence 11, Appli
36	1217	58.3	437	2	US-09-293-505-14	Sequence 14, Appli
37	1217	58.3	437	2	US-08-957-874-11	Sequence 11, Appli
38	1217	58.3	437	2	US-09-325-256-20	Sequence 20, Appli
39	1217	58.3	437	2	US-09-639-695-11	Sequence 11, Appli
40	1217	58.3	437	2	US-09-448-188-11	Sequence 11, Appli
41	1217	58.3	437	2	US-08-954-128-11	Sequence 11, Appli
42	1217	58.3	437	2	US-09-704-917-13	Sequence 13, Appli
43	1217	58.3	437	2	US-08-954-740-11	Sequence 11, Appli
44	1217	58.3	437	2	US-09-151-999-13	Sequence 13, Appli
45	1217	58.3	437	2	US-09-736-476-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
 US-09-325-256-24
 ; Sequence 24, Application US/09325256
 ; Patent No. 6444793
 ; GENERAL INFORMATION:
 ; APPLICANT: PEPINSKY, R. BLAKE
 ; APPLICANT: BAKER, DARREN P.
 ; APPLICANT: WEN, DINGYI
 ; APPLICANT: WILLIAMS, KEVIN P.
 ; APPLICANT: GARGER, ELLEN A.
 ; APPLICANT: TAYLOR, FREDERICK R.
 ; APPLICANT: GALDES, ALPHONSE
 ; APPLICANT: PORTER, JEFFREY
 ; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; FILE REFERENCE: BIV-067.01
 ; CURRENT APPLICATION NUMBER: US/09/325,256
 ; CURRENT FILING DATE: 1999-06-03
 ; PRIOR APPLICATION NUMBER: 60/099,800
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/078,935
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/089,685
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/067,423
 ; PRIOR FILING DATE: 1997-12-03
 ; PRIOR APPLICATION NUMBER: PCT/US98/25676
 ; PRIOR FILING DATE: 1998-12-03
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 396
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-325-256-24

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2006, 11:51:45 ; Search time 181 Seconds
 (without alignments)
 1013.442 Million cell updates/sec

Title: US-08-900-220C-17

Perfect score: 2088

Sequence: 1 MALLTNLLPLCCLALLALPA.....PTGMHWYSRLLYRLAELLG 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	2088	100.0	396	2	US-08-900-220C-17	Sequence 17, Appl
2	2088	100.0	396	3	US-09-151-999-17	Sequence 17, Appl
3	2088	100.0	396	3	US-09-883-848A-17	Sequence 17, Appl
4	2088	100.0	396	3	US-09-187-387-17	Sequence 17, Appl
5	2088	100.0	396	3	US-09-827-110-17	Sequence 17, Appl
6	2088	100.0	396	3	US-09-845-025C-17	Sequence 17, Appl
7	2088	100.0	396	3	US-09-451-939-17	Sequence 17, Appl
8	2088	100.0	396	3	US-09-238-243-17	Sequence 17, Appl
9	2088	100.0	396	3	US-09-795-917-17	Sequence 17, Appl
10	2088	100.0	396	4	US-10-294-036-17	Sequence 17, Appl
11	2088	100.0	396	4	US-10-244-095A-17	Sequence 17, Appl
12	2088	100.0	396	4	US-10-275-107-40	Sequence 40, Appl
13	2088	100.0	396	4	US-10-652-298A-17	Sequence 17, Appl
14	2088	100.0	396	4	US-10-727-195-17	Sequence 17, Appl
15	2088	100.0	396	5	US-10-665-923-17	Sequence 17, Appl
16	2088	100.0	396	5	US-10-652-686-17	Sequence 17, Appl
17	2088	100.0	396	5	US-10-658-745-17	Sequence 17, Appl
18	2088	100.0	396	5	US-10-989-649-4	Sequence 4, Appli
19	2088	100.0	396	5	US-10-505-230-1	Sequence 1, Appli
20	2088	100.0	396	6	US-11-018-739-17	Sequence 17, Appl
21	2088	100.0	396	6	US-11-061-863-17	Sequence 17, Appl
22	2083	99.8	396	4	US-10-147-463-3	Sequence 3, Appli
23	2081	99.7	396	3	US-09-244-466-2	Sequence 2, Appli
24	2008	96.2	396	2	US-08-900-220C-11	Sequence 11, Appl
25	2008	96.2	396	2	US-08-954-771-9	Sequence 9, Appli
26	2008	96.2	396	2	US-08-462-386D-9	Sequence 9, Appli
27	2008	96.2	396	3	US-09-021-660A-35	Sequence 35, Appl
28	2008	96.2	396	3	US-09-151-999-11	Sequence 11, Appl
29	2008	96.2	396	3	US-09-990-046-13	Sequence 13, Appl
30	2008	96.2	396	3	US-09-733-634-22	Sequence 22, Appl
31	2008	96.2	396	3	US-09-883-848A-11	Sequence 11, Appl

32	2008	96.2	396	3	US-09-187-387-11	Sequence 11, Appl
33	2008	96.2	396	3	US-09-827-110-11	Sequence 11, Appl
34	2008	96.2	396	3	US-09-845-025C-11	Sequence 11, Appl
35	2008	96.2	396	3	US-09-451-939-11	Sequence 11, Appl
36	2008	96.2	396	3	US-09-238-243-11	Sequence 11, Appl
37	2008	96.2	396	3	US-09-736-476-9	Sequence 9, Appli
38	2008	96.2	396	3	US-09-795-917-11	Sequence 11, Appl
39	2008	96.2	396	4	US-10-294-036-11	Sequence 11, Appl
40	2008	96.2	396	4	US-10-244-095A-11	Sequence 11, Appl
41	2008	96.2	396	4	US-10-456-954-14	Sequence 14, Appl
42	2008	96.2	396	4	US-10-414-267-14	Sequence 14, Appl
43	2008	96.2	396	4	US-10-652-298A-11	Sequence 11, Appl
44	2008	96.2	396	4	US-10-727-195-11	Sequence 11, Appl
45	2008	96.2	396	5	US-10-665-923-11	Sequence 11, Appl

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2006, 11:51:58 ; Search time 15 Seconds
 (without alignments)
 294.026 Million cell updates/sec

Title: US-08-900-220C-17

Perfect score: 2088

Sequence: 1 MALLTNLLPLCCLALLALPA.....PTGMHWYSRLLYRLAELLG 396

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	812.5	38.9	225	7	US-11-254-524-56			Sequence 56, Appl
2	95.5	4.6	1039	6	US-10-511-937-2429			Sequence 2429, Ap
3	87.5	4.2	356	6	US-10-953-349-31730			Sequence 31730, A
4	84	4.0	216	6	US-10-953-349-34129			Sequence 34129, A
5	84	4.0	227	6	US-10-953-349-34128			Sequence 34128, A
6	80.5	3.9	448	7	US-11-293-697-3667			Sequence 3667, Ap
7	80	3.8	143	6	US-10-953-349-34130			Sequence 34130, A
8	80	3.8	373	6	US-10-953-349-34278			Sequence 34278, A
9	80	3.8	1443	7	US-11-293-697-3844			Sequence 3844, Ap
10	78.5	3.8	310	6	US-10-953-349-24588			Sequence 24588, A
11	78.5	3.8	331	6	US-10-953-349-26692			Sequence 26692, A
12	78.5	3.8	342	6	US-10-953-349-26691			Sequence 26691, A
13	78.5	3.8	399	6	US-10-953-349-24587			Sequence 24587, A
14	78.5	3.8	408	6	US-10-953-349-24586			Sequence 24586, A
15	78	3.7	213	6	US-10-953-349-13254			Sequence 13254, A
16	78	3.7	543	6	US-10-953-349-31946			Sequence 31946, A
17	77	3.7	213	6	US-10-953-349-23632			Sequence 23632, A
18	76.5	3.7	727	6	US-10-505-928-644			Sequence 644, App
19	76.5	3.7	727	6	US-10-511-937-2606			Sequence 2606, Ap
20	76	3.6	296	6	US-10-953-349-35299			Sequence 35299, A
21	75.5	3.6	328	6	US-10-953-349-32429			Sequence 32429, A
22	75.5	3.6	383	6	US-10-953-349-3321			Sequence 3321, Ap
23	75.5	3.6	388	6	US-10-953-349-3320			Sequence 3320, Ap
24	75.5	3.6	448	7	US-11-293-697-4755			Sequence 4755, Ap
25	75	3.6	352	6	US-10-953-349-34763			Sequence 34763, A
26	75	3.6	356	6	US-10-953-349-34762			Sequence 34762, A
27	75	3.6	956	7	US-11-293-697-3037			Sequence 3037, Ap
28	74.5	3.6	526	6	US-10-953-349-32170			Sequence 32170, A
29	74	3.5	3011	7	US-11-236-836-14			Sequence 14, Appl

30	73.5	3.5	387	6	US-10-953-349-31151	Sequence 31151, A
31	73.5	3.5	792	6	US-10-953-349-8716	Sequence 8716, Ap
32	73.5	3.5	806	6	US-10-953-349-8715	Sequence 8715, Ap
33	73.5	3.5	825	6	US-10-953-349-8714	Sequence 8714, Ap
34	73.5	3.5	1394	6	US-10-953-349-6031	Sequence 6031, Ap
35	73.5	3.5	1407	6	US-10-953-349-6030	Sequence 6030, Ap
36	73.5	3.5	1408	6	US-10-953-349-6029	Sequence 6029, Ap
37	73	3.5	317	6	US-10-953-349-26693	Sequence 26693, A
38	73	3.5	335	6	US-10-953-349-28468	Sequence 28468, A
39	73	3.5	392	6	US-10-953-349-5493	Sequence 5493, Ap
40	73	3.5	418	6	US-10-953-349-5492	Sequence 5492, Ap
41	73	3.5	499	6	US-10-953-349-30898	Sequence 30898, A
42	73	3.5	501	6	US-10-953-349-30897	Sequence 30897, A
43	73	3.5	570	6	US-10-953-349-32501	Sequence 32501, A
44	73	3.5	577	6	US-10-953-349-32500	Sequence 32500, A
45	73	3.5	581	6	US-10-953-349-32499	Sequence 32499, A